

#### REMARKS

In response to Notice of Non-Compliant Amendment, Applicants herewith submit Replacement and annotated sheets for Figure 1-23, indicating changes in pagination. Each of the new figures 19-24 is indicated as "New Sheet". These new figures were referred to in the response to the Office Action submitted on November 20, 2006. Thus, no new matter is added.

The Examiner is invited to contact the undersigned at (914) 712-0093 if there are any questions about this amendment or application.

Respectfully submitted,

Date: 4/17/08

Cheryl H. Agris, Reg. No. 34,086



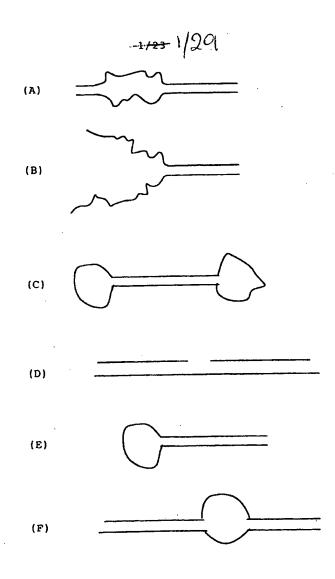


Figure 1 (A-F)

Construct Forms Comprising at Least one Single-Stranded Region

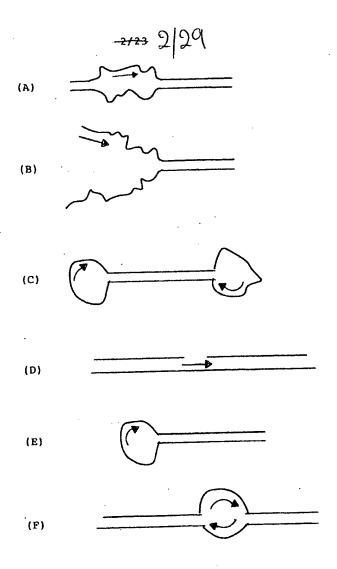
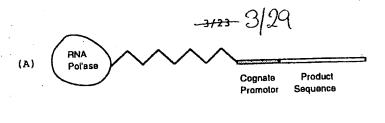
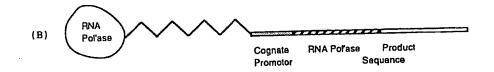


Figure 2 (A-F)

Functional Forms of the Construct





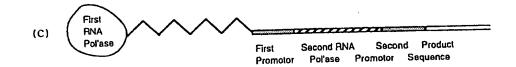


Figure 3 (A-C)

Three Constructs with an RNA Polymerase Covalently Attached to a Transcribing Cassette

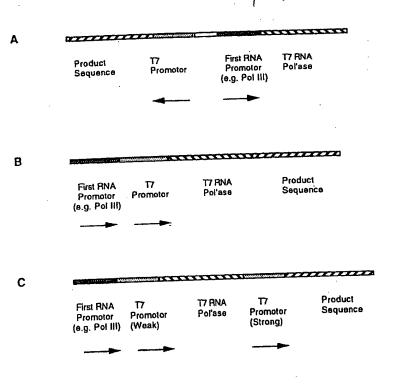


Figure 4 (A-C)

Three Constructs with Promoters for Endogenous RNA Polymerase

M13mp18. Seq Length: 7250 AATTGATGCC ACCTTTTCAG CTOGCGCCCC AATGCTACTA CTATTAGTAG ATAGCTAAAC AGGITATIGA CCATTIGCGA AATGTATCTA AAATGAAAAT **AACTGTTACA** OGTTOGCAGA ATTEGGAATC TAAATCTACT **ATGGTCAAAC** GTTGCATATT TAAAACATGT COGTACTTTA CTTCCAGACA TOGAATGAAA AGCAATTAAG CTCTAAGCCA CACCAGATTC TGAGCTACAG: 201 CAATTAAAGG TACTCTCTAA TOCTGACCTG TCAAAAGGAG **TGACCTCTTA** TTAAAACGCG GGITTOGCTTT GAAGCTOGAA CTTCCCGCTCT TTGGAGTTTG TTCCTCTTAA. TCTTTTTGAT **GCAATCCGCT** TCTTTCCGGC **ATATTTGAAG** CAGGGTAAAG ACCTGATTTT **TGATTTATGG** CTATAATAGT TTGCTTCTGA **ATTCAATGAA** GTTTAAAGCA TTTGAGGGGG TTTCTGAACT **TCATTCTCGT** TATTOGACGC TATCCAGTCT **AAACATTITA** GATTOOGCAG **TATTTATGAC** 501. CAAAAGCCTC TOGCTATTTT CTCTGGCAAA ACTTCTTTTG CTATTACCCC TTGCTCTTAC GIOGICIEGI AAAOGAGEGT TATGATAGTG **GGTTTTTATC ATCTGCATTA** AATTCCTTTT **GCCCTTATGT** TATGCCTCGT CTACCTGTAA ATGAATCTTT **ATCTCAACTG GTATTCCTAA** GTCCTGACTG TCTTOCCAAC **GTTTTATTAA** CGTAGATTTT COGTTAGTTC **AGGTAATTCA** CCAGTTCTTA AAATCGCATA **GTATAATGAG** TCTGGTGTTC **TACTACTOGT AAACCATCTC** AAGCCCAATT **AGTTGAAATT** TACGITGATT **GCAGCTITIGT** CACTGAATGA AAGCTTATT TOGTCAGGGC ATGAAGGTCA CITGITOGAAG **ATTACTCTTG ATATOOGGTT** TEGETAATGA TCTTTCAAAG TGTACACCGT **TCATCTGTCC** COCCUCIOGIC 1001 GOCAGOCTAT GICIGOGOCT COTTOCCGCT **ATGATTGACC** 1051 TTGGTCAGTT **CEGTICCCIT** CAGGOGATGA CACAATTTAT GAGCAGGTCG **CGGATTTCGA** 1101 AAGTAACATG OGTIGIACCTT TGTTTOGCGC TTGGTATAAT **OCCIGORAGI** 1151 TACAAATCTC CCTCTTTCGT TTTAGGTTGG 1201 CAAAGATGAG TGTTTTAGTG TATTCTTTCG

Figure 5

6/23 6/29

1251	TGCCTTCGTA	GTGGCATTAC	GTATTTTACC	OGTITAATGG	AAACTTCCTC
1301	ATGAAAAAGT	CTTTAGTCCT	CAMAGOCTICT	GTAGCCGTTG	CTACCCTCGT
1351	TOOGATGCTG	TCTTTCGCTG	CTGAGGGTGA	OGATICCCOGCA	AAAGOGGOCT
1401	TTAACTCCCT	GCAAGCCTCA	COCACOGAAT	ATATOGGTTA	TEOGTEGGGG
1451	ATGGTTGTTG	TCATTGTCGG	COCAACTATC	<b>GGTATCAAGC</b>	TGTTTAAGAA
1501	ATTICACCTICG	AAAGCAAGCT	GATAAACOGA	TACAATTAAA	GCTCCTTTT
1551	<b>GGAGOCTTTT</b>	TTTTTGGAGA	TTTTCAACGT	GAAAAAATTA	TTATTOGCAA
1601	TTCCTTTAGT	TGTTOCTTTC	TATTCTCACT	COCCTGAAAC	TGTTGAAAGT
1651	TGTTTAGCAA	AACCCCATAC	AGAAAATTCA	TTTACTAACG	TCTGGAAAGA
1701	OGACAAAACT	TTAGATOGTT	ACGCTAACTA	TGAGGGTTGT	CTGTGGAATG
1751	CTACAGGCGT	TGTAGTTTGT	ACTEGTGACG	AAACTCAGTG	TTACGGTACA
1801	TEGETTOCTA	Песеспес	TATOCCTGAA	AATGAGGGTTG	GTEGETICTEA
1851	व्यवाख्यव्या	TCTGAGGGTG	GOGGTTCTGA	<b>COGTICACOGIT</b>	ACTAMACCTC
1901	CTGAGTACGG	TGATACACCT	ATTOOGGGCT	ATACTTATAT	CAACCCTCTC
195	1 GACGGCACTT	ATCCCCCTGG	TACTGAGCAA	AACCCCCTA	ATOCTAATOC
200		GAGTCTCAGC	CTCTTAATAC	TTTCATGTTT	CAGAATAATA
205	1 GCTTCCGAAA	TAGGCAGGGG	GCATTAACTG	TTTATACGGC	CACTGTTACT
210			AACTTATTAC	CAGTACACTC	CTGTATCATC
215		TATGACGCTT	ACTEGAACEG	TAAATTCAGA	GACTGOGCTT
220			AACTTATTAC	CAGTACACTO	CTGTATCATC
215		_	TOCTGTCAAT	GCIGGGGGGG	actic tegrings
220			GATOCATTO	TTTGTGAATA	TCAAGGCCAA
225			TOCTGTCAAT	CELEGGEGGG	eciciegieg
230			AGGGIGGIGG	CICIGAGGG	r ecocentricie
235			A GEOGETIOO	GIEGIEGE	тесттоосст
	1 GATTTIGAT		T GGCAAACGC	DEDEDBAATAA T	G CTATGACCGA
	5 1 AAATGOOGA		C TACAGTOTG	A COCTAMAGO	C AAACTTGATT
241	, ,,,,,		Floure 5		

Figure 5

7/23 7/29

2501	CTGTCGCTAC	TGATTACGGT	<b>GCTGCTATCG</b>	ATGGTTTCAT	TOGTGACGIT
2551	TOOGGOOTTG	CTAATGGTAA	TOGTOCTACT	GGTGATTTTG	CTGGCTCTAA
2601	TTOOCAAATG	CCTCAAGTCG	GTGACCETGA	TAATTCACCT	TTAATGAATA
2651	ATTTOOGTCA	ATATTTACCT	TOOCTOOCTC	AATOGGTTGA	ATCTCCCCCT
2701	ППСТПТА	GOGCTGGTAA	ACCATATGAA	TTTTCTATTG	ATTIGTGACAA
2751	AATAAACTTA	TICOGIEGIG	TCTTTGCGTT	TCTTTTATAT	GTTGCCACCT
2801	TTATGTATGT	ATTTTCTACG	TTTGCTAACA	TACTGOGTAA	TAAGGAGTCT
2851	TTATCATGCC	AGTTCTTTTG	<b>CETATTOCET</b>	TATTATTGCG	THOCTOGGT
2901	поспстес	TAACTTTGTT	<b>COOCTATCTG</b>	CTTACTTTTC	TTAAAAAGGG
2951	CTTCGGTAAG	ATAGCTATTG	CTATTTCATT	GTTICTTGCT	CTTATTATTG
3001	<b>CECTTAACTC</b>	AATTCTTGTG	GGTTATCTCT	CTGATATTAG	OGCTCAATTA
3051	COCTCTGACT	TIGITCAGGG	TGTTCAGTTA	ATTICTCCCGT	CTAATGCGCT
3101	TCCCTGTTTT	TATGTTATTC	TCTCTGTAAA	GGCTGCTATT	TTCATTTTTG
3151	ACGITTAAACA	AAAAATOGTT	TCTTATTTGG	ATTGGGATAA	ATAATATGGC
3201	TGTTTATTTT	GTAACTGGCA	AATTAGGCTC	TEGAAAGACG	CTOGTTAGOG
3251	TTGGTAAGAT	TCAGGATAAA	ATTGTAGCTG	<b>GGTGCAAAAT</b>	AGCAACTAAT
	CTTGATTTAA	GGCTTCAAAA	OCTOCOGCAA	GTCGGGAGGT	TOGCTAAAAC
3351	COCTOCOGIT	CTTAGAATAC	COGGATAAGCC	TTCTATATCT	GATTTGCTTG
3401	CTATTGGGGG	COGTAATGAT	TOCTACGAATO	AAAATAAAA 2	COCCTTCCTT
345	GTTCTCGATG	AGTGCCGTAC	TTGGTTTAAT	ACCOGNICIT	GGAATGATAA
350	1 GGAAAGACAG	COGATTATTG	ATTGGTTTCT	ACTECTOGT	AAATTAGGAT
355	1 GGGATATTAT	ппспеп	CAGGACTTAT	CTATTGTTGA	TAAACAGGCG
360	1 CGTTCTGCAT	TAGCTGAACA	TGTTGTTTAT	TGTCGTCGTC	TOGACAGAAT
365	1 TACTTTACCT	TITGTOGGTA	CTTTATATTC	TCTTATTACT	GGCTCGAAAA
370	1 TEOCTICTECC	; TAAATTACAT	- Gilecocile	TTAAATATGG	CGATTCTCAA
375	1 TTAAGCOCTA	CTGTTGAGOG	TTGGCTTTAT	ACTEGTAAGA	ATTTGTATAA
380		CTANACAGO	CTTTTCTAG	TAATTATGAT	TOOOGTGTTT
			<b>=</b> :		

Figure 5

8/23 8/29

3851	ATTCTTATTT	AACGCCTTAT	TTATCACACG	GTOGGTATTT	CAAACCATTA
3901	AATTTAGGTC	AGAAGATGAA	ATTAACTAAA	ATAATATTGA	AAAAGTTTTC
3951	TOGOGTTCTT	TGTCTTGOGA	TTGGATTTGC	ATCAGCATTT	ACATATAGTT
4001	ATATAACCCA	ACCTAAGOOG	GAGGTTAAAA	AGGTAGTCTC	TCAGACCTAT
4051	GATTTTGATA	AATTCACTAT	TGACTCTTCT	CAGCGTCTTA	ATCTAAGCTA
4101	TOGCTATGTT	TTCAAGGATT	CTAAGGGAAA	ATTAATTAAT	AGOGACGATT
4151	TACAGAAGCA	AGGTTATTCA	CTCACATATA	TTGATTTATG	TACTGTTTCC
4201	ATTAAAAAAG	GTAATTCAAA	TGAAATTGTT	AAATGTAATT	AATTTTGTTT
4251	TCTTGATGTT	TGTTTCATCA	тсптспппа	CTCAGGTAAT	TGAAATGAAT
4301	AATTOGOCTC	TGCGCGATTT	TGTAACTTGG	TATTCAAAGC	AATCAGGGGA
4351	AATCCGTTATT	GITTCTCCCCG	ATGTAAAAGG	TACTGTTACT	GTATATTCAT
4401	CTGACGTTAA	ACCTGAAAAT	CTACGCAATT	TCTTTATTTC	TGTTTTACGT
4451	GCTAATAATT	TTGATAATGGT	TGGTTCAATT	OCTTOCATAA	TTCAGAAGTA
	TAATOCAAAC	AATCAGGATT	ATATTGATGA	.ATTGCCATCA	TCTGATAATC
	AGGAATATGA	TGATAATTCC	<b>ectochicis</b>	वाद्यागटा	TGTTCCGCAA
4601	AATĢATAATG	TTACTCAAAC	TTTAAAATT	AATAACGTTC	GGGCAAAGGA
465	I TITAATAOGA	GTTGTCGAAT	TGTTTGTAAA	GTCTAATACT	TCTAAATCCT
470	1 CAAATGTATT	ATCTATTGAC	<b>GECTICTAATC</b>	TATTAGTTGT	TAGTGCTCCT
475	1 AAAGATATTT	TAGATAACCT	TOCTCAATTC	CTTTCTACTG	TTGATTTGCC
480	1 AACTGAOCAG	ATATTGATTG	AGGITTGAT	ATTTGAGGIT	CAGCAAGGTG
485	1 ATGCTTTAGA	TTTTCATT	ectectesct	CTCAGOGTGG	CACTGTTGCA
490	1 GEOGGIGITA	ATACTGACCG	OCTCAOCTCT	GTTTTATCTT	CIECTEGIEG
495			GOGATGTTTT	AGGGCTATCA	GTTCGCGCAT
500			AAAATATTGT	CIGIGOCACG	TATTCTTACG
505			TATCTCTGT	r ggocagaatg	TCCCTTTTAT
510			- AAAATATTG	CTGTGCCACC	TATTCTTACG
515				A TGAGOGTTT	T TOCTIGITIGEA
312	,	•			

-Figure 5

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				*****	COGATAGTTT
5201	ATGGCTGGGG.	GTAATATTGT	TCTGGATATT	ACCAGCAAGG	
5251	GAGTTCTCT	ACTCAGGCAA	GTGATGTTAT	TACTAATCAA	AGAAGTATTG
5.301	CTACAACGGT	TAATTTGOGT	GATGGACAGA	CTCTTTTACT	COGIGOCOCTC
5351	ACTGATTATA	AAAACACTTC	TCAAGATTCT	GEOGTACOGT	TOCTGTCTAA
5401	AATCCCTTTA	ATCOGCCTCC	TGTTTAGCTC	COCCTCTGAT	TOCAACGAGG
5451	AAAGCACGTT	ATACGTGCTC	GTCAAAGCAA	CCATAGTACG	COCCTGTAG
5501	COCCCCATTA	ACCOCCCCCCC	दादाख्दाख्दा	TACGCGCAGC	GTGACCECTA
	CACTTGCCAG	COCCTAGCG	COORCITOCIT	TOGCITICIT	σοποσπί
5601	CTOGOCAOGT	TOGCOGGCTT	TOOOGTCAA	GCTCTAAATC	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	TITAGGGTTC	CGATTTAGTG	CTTTACGGCA	CCTCCGACCCCC	AAAAAACTTG
5701	ATTTGGGTGA	TEGTTCACGT	AGTGGGCCAT	<b>CGCCCTGATA</b>	GACGGTTTTT
	CCCCTTTGA	CGTTGGAGTC	CACGITICITT	AATAGTGGAC	TCTTGTTCCA
	AACTGGAACA	ACACTCAACC	CTATCTOGGG	CTATTCTTTT	GATTTATAAG
	GGATTTTGCC	GATTTOGGAA	CCACCATCAA	ACAGGATTTT	COCCIOCIOS
	COCAMACCAG	CGTTGGACCCC	TTGCTGCAAC	TCICTCAGGG	CCAGGOGGTG
	AAGGGCAATC	AGCTGTTGCC	OGICIOGCIG	GTGAAAAGAA	AAAOCAOOCT
600			CTCTCCCCG	CECCITECEC	GATTCATTAA
605	1 TGCAGCTGGC	ACGACAGGTT	TOOOGACTEG	AAAGCGGGGCA	GTGAGOGCAA
610	1 COCAATTAAT	GTGAGTTAGC	TCACTCATTA	GGCACCCAG	<b>GCTTTACACT</b>
615			TIGIGIGGAA	TIGIGAGOGG	ATAACAATTT
620	1 CACACAGGAA	ACAGCTATGA	CCATGATTAC	GAATTOGAGO	TOGGTACCOG
	1 GOGATOCTC		TOCAGOCATO	CAAGCTTGGC	ACTEGEOCGTC
	1 GTTTTACAAC		GGAAAACCCT	COOGITACOO	AACTTAATOG
	1 OCTTGCAGC		TOGOCAGCTO	GOGTAATAGO	CAACACCCCCC
	1 GCACCGATCO		A CÄGILIGOGO	A GOCTGAATGO	CGAATGGCGC
		T TTCCGGCAC	AGAAGOGGTO	G COORGANAGE	COCTOCAGTG
	1 CGATCTTCC			T COOCTCANN	TEGCAGATEC
US.	,, 00	•			•

Figure 5

### 10/23 10/29

6651	ACGGTTACGA	TGCGCCCATC	TACACCAACG	TAAOCTATOC	CATTACCGTC
	AATCOGOOGT	TIGTTCCCAC	CCACAATOOG	ACGCCTTCTT	ACTOGCTCAC
-		GATGAAAGCT	GOCTACAGGA	ACCOCAGACG	CGAATTATTT
		TOCTATIGGT	TAAAAAATGA	<b>GCTGATTTAA</b>	CAAAAATTTA
6751	ACCCCAATTT	TAACAAAATA	TTAACGTTTA	CAATTTAAAT	ATTTGCTTAT
6001	ACAATCTTCC	TGTTTTGGG	GCTTTICTGA	TTATCAACOG	GGGTACATAT
		CTAGTTTTAC			CTTGTTTGCT
6001	CAGACTICTC	AGGICAATIGAC	CTGATAGOCT	TTGTAGATCT	CTCAAAAATA
6051	CCTACOCTCT	COGGCATGAA	TTTATCAGCT	AGAACEGTTG	AATATCATAT
7001	TGATGGTGAT	TTGACTGTCT	COCCCCTTTC	TCACCCTTTT	GAATCTTTAC
7051	CTACACATTA	CTCAGGCATT	GCATTTAAAA	TATATGAGGG	TTCTAAAAAT
710	TTTTATCCTT	COCTTGAAAT	AAAGGCTTCT	CCCCCAAAAG	TATTACAGGG
710	+ TOATAATGIT	TITGGTACAA	COGATTTAGC	TITATGCTCT	GAGGCTTTAT
/15	I IONIMICIT				

Figure 5

11/23 11/29

#### COMPLEMENTARY TO M13

POSITION 6 4 5	5' 3' AGCAACACTATCATA	POSITION 631	M <sub>13</sub> /1
615	ACGACGATAAAAACC	601	M <sub>13</sub> /2
585	TTTTGCAAAAGAAGT	571	M <sub>13</sub> /3
555	AATAGTAAAATGTTT	541	M <sub>13</sub> /4
525	CAATACTGOGGAATG	511	M <sub>13</sub> /5
495	TGAATOCCCTCAAA	481	M <sub>13</sub> /6
465	AGAAAAOGAGAATGA	451	M <sub>13</sub> /7
435	CAGGTCTTTACCCTG	421	M <sub>13</sub> /8
405	AGGAAAGCGGATTGC	391	M <sub>13</sub> /9
375	AGGAAGOOOGAAAGA	361	M <sub>13</sub> /10

#### COMPLEMENTARY TO SS PHAGE DNA

POSITION	•	POSITION	
,	5' 3' ATATTTGAAGTCTTT	366	M <sub>13</sub> /11
351	• •	386	M <sub>13</sub> /12
371	TCTTTTTGATGCAAT	380	
391	CTATAATACTCAGGG	406	M <sub>13</sub> /13
411	TGATTTATGGTCATT	426	· M <sub>13</sub> /14
431	GTTTAAAGCATTTGA	446	M <sub>13</sub> /15
451	TATTTATGACGATTC	466	M <sub>13</sub> /16
471	TATCCAGTCTAAACA	486	M <sub>13</sub> /17
491	CTCTGGCAAAACTTC	506	M <sub>13</sub> /18
511	TOGOTATTTTGGTTT	526	M <sub>13</sub> /19
·531	AAACGAGGGTTATGA	546	M 13/20

Figure 6

Primers for Nucleic Acid Production Derived from M13mp18 Sequence

12/23 12/29

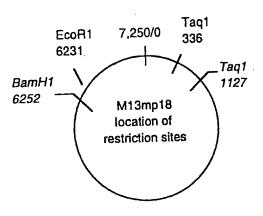


Figure 7

Appropriate M13mp18 Restriction Sites

13/23 13/20



Lane 1: from calf thymus + Taq digested mp18 amplification reaction

Lane 2: from Taq digested mp18 amplification reaction

Lane 3: from calf thymus amplification reaction

Lane 4: øX174 Hinf1 size marker

Figure 8

14/23 14/29



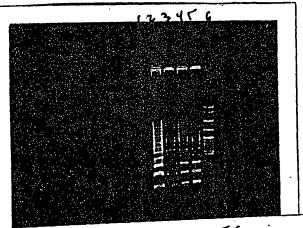
Lane 1: no template

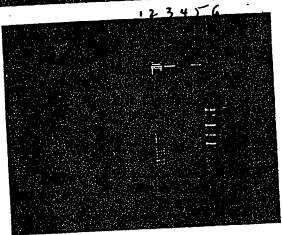
Lane 2: mp18 template, phosphate buffer

Lane 3: Mspl/pBR322 size marker Lane 4: mp18 template, MOPS buffer

Figure 9

## 15/23 15/29





Top= (+) Template
Bottom= (-) Template

Lane 1: phosphate buffer

Lane 2: MES Lane 3: MOPS Lane 4: DMAB Lane 5: DMG

Lane 6: pBR322/Mspl size marker

Figure 10

16/23 16/29



Lane 1: DMAB buffer, no template

Lane 2: DMAB buffer, mp18 template

Lane 3: DMG buffer, no template

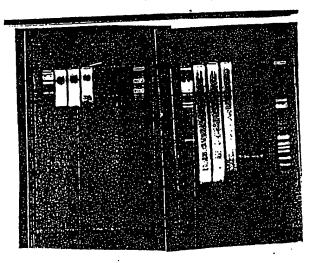
Lane 4: DMG buffer, mp18 template

Lane 5: No reaction

Lane 6: 200 ng Taq I digested mp18 size marker/positive control

Figure 11

### 17/23 17/29



Second Time Interval First Time Interval

#### Agarose Gel Analysis

Lane 1: lambda Hind III marker

Lane 2: Amp/Untreated

Lane 3: Amp/Kinased

Lane 4: Amp/Kinased/Ligated

Lane 5: PCR/Untreated

Lane 6: PCR/Kinased

Lane 7: PCR/Kinased/Ligated Lane 8: øX174/Hinf1 marker

Figure 12

18/23 18/29

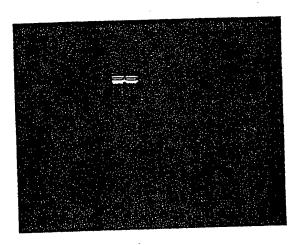
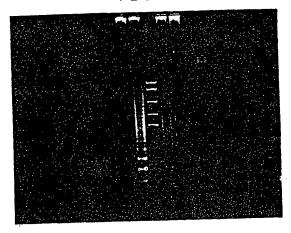


Figure 13

19/23 19/29

1 2 3 4 5 6



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

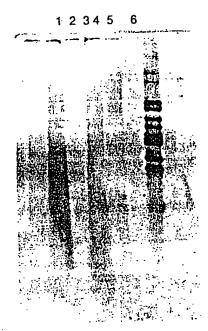
Lane 4: Primers + RNA
Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 14

20/23 20/29



Lane 1: Primers alone

Lane 2: Primers + taq digested M13 DNA

Lane 3: Molecular weight markers

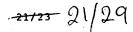
Lane 4: Primers + RNA

Lane 5: Primers alone

Lane 6: M13 digested DNA

Buffer was dimethyl amino glycine, pH 8.6

Figure 15



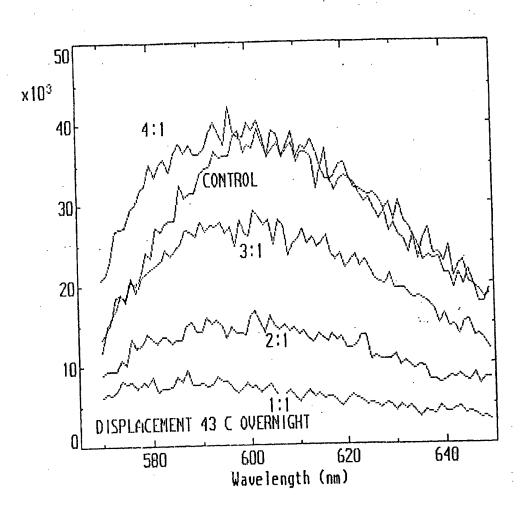
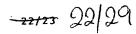


Figure 16



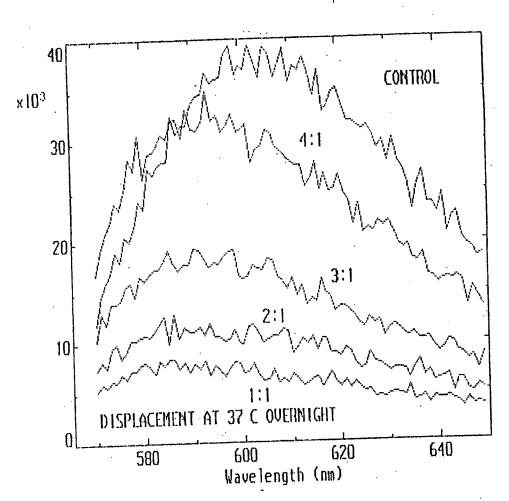


Figure 17

-23/23 23/29

pIBI 31-BH5-2

fmet AUG of Lac z

LAC PROMOTOR.ATG ACC ATG ATT ACG CCA GAT ATC AAA TTA ATA CGA CTC ACT ATA

Oligo 50-mer

3'- tac t\*aa t\*gc ggt\* ct\*a t\*ag t\*Vt aat\* tat\* gct\* gag t\*ga t\*at\* c-5\*

10 base insert

T7 RNA Start («« T3 Promotor Region )
IGGG CTC ICCT TTA GTG ACG GTT AAT
....») «- T3 Start Signal

#### pIBI 31 BSII/HCV

("- T7 Promotor Region )

MULTIPLE CLONING SITE + 390 BASE INSERT CTA /TAG TGA GTC CGT ATT AAT....

"- T7 Start Signal

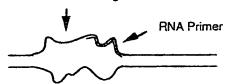
5'-ct'a t'ag t'ga gt'c gt'a tt'a at'..........

24/29

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 				•	_	_	 		_	_ `	_	_		_			_	-	 	· -	 -	 -	 -	-	•	-		-		 	• -		2
 -	-	_	-	-	_											_	_	_	 		 -	 	 . <b>-</b>	-			•		-	 		-	J
 -	-	_	-		-	-	 -	-	-	_	_			_	_																		

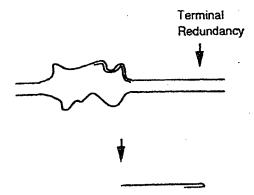
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Replication Bubble with Nucleotide Analogs



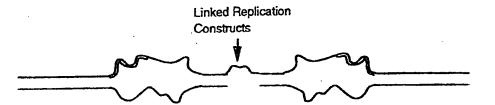
Primer-Dependent DNA Production Using Nucleic Acid Construct

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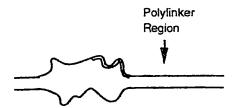
Hairpin Product

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Linked Complementary Production Constructs

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Cloning Site in Production Constructs

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#### ARRANGEMENT OF OLIGONUCLEOTIDE PRIMERS IN AMPLIFICATION REACTION

1	2	3	4	5	6	7	8	9	10
20	19	18	17	16	15	14	13	12	11